

We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

6,900

Open access books available

186,000

International authors and editors

200M

Downloads

Our authors are among the

154

Countries delivered to

TOP 1%

most cited scientists

12.2%

Contributors from top 500 universities



WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index
in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com



Neglected and Underutilized Legume Crops: Improvement and Future Prospects

Jacob Popoola, Omena Ojuederie, Conrad Omonhinmin and Adegoke Adegbite

Abstract

Sustainable agricultural productivity is hampered by over-dependency on major staple crops, neglect and underutilization of others, climate change, as well as land deterioration. Challenges posed by these limiting factors are undoubtedly contributing to global food insecurity, increased rural poverty, and malnutrition in the less developed countries. Miscellaneous neglected and underutilized grain legumes (MNUGLs) are crops primarily characterized by inherent features and capabilities to withstand the effects of abiotic stress and climate change, significantly replenish the soil, as well as boost food and protein security. This chapter provides insight into the benefits of MNUGLs as food and nutritional security climate smart crops, capable of growing on marginal lands. Exploring and improving MNUGLs depend on a number of factors among which are concerted research efforts, cultivation and production, as well as utilization awareness across global populace geared toward reawakening the interest on the abandoned legumes. The emergence of the clustered regularly interspaced short palindromic repeat (CRISPR/cas9) technology combined with marker-assisted selection (MAS) offers great opportunities to improve MNUGLs for sustainable utilization. Advances in improvement of MNUGLs using omic technologies and the prospects for their genetic modification were highlighted and discussed.

Keywords: climate change, CRISPR/cas9, food security, marker-assisted selection (MAS), omic technologies, underutilized grain legumes

1. Introduction

The world is confronted with the challenges of climate change, terrorism, and poverty, among other factors, which hinder food production, food availability, as well as food and nutritional security. Globally, food insecurity and low supply in many areas are threatening the human population and survival in the areas where terrorism and transborder and internal displacement of persons are entrenched in many parts of the world. Food as an important commodity for survival is under threat, and if survival strategies are not devised, the catastrophe will be overbearing. A number of crop species are becoming extinct from our agricultural and forest fields, while some others are declining both in cultivation and utilization. A review of global food security indicates re-strategizing crop genetic improvement and production agronomy toward grain legumes to identify climate-resilient species and

varieties with enhanced grain features [1, 2]. This is highly desirable considering the significant roles that grain legumes play in the food cultures around the world as veritable sources of quality protein, natural medicine, animal fodder, natural fertilizers, and environmental restoration products, alongside the well-established soil enrichment property of symbiosis with nitrogen-fixing bacteria [3].

In order to meet the global food demands, focus should be on promoting the cultivation and utilization of other crops which have been neglected and underexploited but have the potential to enhance food and nutrition security especially in the developing countries of sub-Saharan Africa. With the recent negative impact of climate change being experienced globally, Africa is the most affected as a region that depends on rain-fed agriculture. The effect of increased drought on agricultural crops has led to yield reductions at harvest, death of livestock, and loss of income and jobs in some parts of Africa especially in Somalia, Kenya, and Ethiopia. This has drastically increased the level of malnutrition and food insecurity. Most of the staple crops are unable to withstand the harsh environmental changes currently taking place. Nevertheless, miscellaneous neglected and underutilized grain legumes (MNUGLs) are more advantageous over the conventional staple crops. These MNUGLs are often linked to the cultural heritage of their places of origin, well adapted to precise agroecological areas, harsh environments, and marginal lands. They also perform well in traditional production systems with little or no external inputs [4–6].

The chapter will cover some selected minor grain legumes with huge potentials to boost protein security in period of hunger and malnutrition in the sub-Saharan Africa and elsewhere. The species are known by many appellations such as miscellaneous, neglected, underutilized, underexploited, and under-researched, among others. These MNUGLs could be further improved using recent advancements in omic technologies for better acceptance and utilization as well as for improved food security.

2. What are miscellaneous, neglected and underutilized grain legumes (MNUGLs?)

Globally, neglected and underutilized species (NUS) are often identified based on their local usefulness, localized domestication, adaptation coupled with general abandonment by mainstream agricultural researchers, extension services, plant breeders, donors, technology providers, policy- and decision-makers, as well as consumers [2, 6]. NUS are classically identified based on certain criteria which include the following:

1. Local importance in consumption and production systems
2. Adaptation to agroecological niches/marginal areas
3. Representation by ecotypes/landraces
4. Cultivation and utilization based only on indigenous knowledge
5. Rare representation in ex situ collections
6. Uncoordinated attention from national agricultural and biodiversity conservation policies, research, and development
7. Neglect by mainstream market system

In reality and broad consideration, a large percentage of such NUS are underutilized legume crops. As such these legume species are classified as minor grain legumes, though consumed as food and forage crops in many parts of the world. Thus, we can refer to this category of legume crops as MNUGLs. On global distribution, these species are endemic to the tropical regions of the world. Several reports and findings have established that MNUGLs are drought-tolerant, endure and thrive under harsh environments, highly adaptable to varying ecogeographical settings, and withstand or mitigate conditions such as heat, drought, diseases, frost, cold, and insect pest attack [1, 5, 7]. These qualities could be scientifically explored for crop improvement and sustainable utilization. Apart from these good qualities, MNUGLs also contain high-quality proteins and micronutrients which are comparable to those found in conventional legumes. They are also indispensable in crop rotation strategies to fertilize agricultural soils.

3. General background information: grain legumes

Grain legumes belong to the family Fabaceae of the Angiospermae and are considered rich in high-quality proteins with significant impacts on the nutrition, diet, and health of many people across the world. The family Fabaceae is divided into grain legumes and pasture/forage legumes. The grain legumes are grown mainly as pulses providing food for humans, while pasture legumes are cultivated to feed domestic animals. Based on plant utility and economy, legumes are categorized into major and minor species. Major legumes are popular and common with well-established domestication and cultivation, agronomic practices, utilization, and conservation. Examples include soybean (*Glycine max* L.), cowpea (*Vigna unguiculata* L.), groundnut (*Arachis hypogaea* L.), common beans (*Phaseolus vulgaris* L.), pea (*Pisum sativum* L.), and chicken pea (*Cicer arietinum* L.), among others. Minor legumes are less known, less exploited, neglected, and considered underutilized. Several species in this category include winged bean (*Psophocarpus tetragonolobus* L.), pigeon pea (*Cajanus cajan* L.), lablab (*Lablab purpureus* L.), lima bean (*Phaseolus lunatus* L.), jack and sword bean (*Canavalia* sp.), mung bean (*Vigna mungo* L.), bambara groundnut (*Vigna subterranea* L.), marama bean (*Tylosema esculentum* L.), kersting's groundnut (*Kerstingiella geocarpa* Harms), African yam bean (AYB) (*Sphenostylis stenocarpa* Harms), and rice bean (*Vigna angularis* L.). The wild species of the minor grain legumes include kersting's groundnut (*Kerstingiella geocarpa* Harms), marama bean (*Tylosema esculentum*), and the wild *Vigna* species such as *V. ambacensis*, *V. vexillata*, *V. luteola*, *V. oblongifolia*, and *V. racemosa*, among others. These species are found in many African countries and could be exploited for food, medicine, agriculture (as cover crops and fodder), and more importantly for genetic improvement of cowpea and related species [8, 9].

A review of literatures indicated that most of the MNUGLs have been relegated to unimportant underutilized crops grown by the older generation of farmers [5, 10]. Thus, sizeable and valuable genetic resources housed within MNUGLs would have been lost due to neglect and lack of concerted focused research. Several authors have highlighted the usefulness of MNUGLs as food security in lean times as farmers in rural areas make a living on the species [11, 12]. Presently, there is no available genome sequence of MNUGLs species which could be utilized for successful breeding and for specific purposes.

3.1 Brief description on some selected MNUGLs

3.1.1 African yam bean (*Sphenostylis stenocarpa* Ex. A. Rich Harms)

The African yam bean (*Sphenostylis stenocarpa*) with somatic chromosome number $2n = 22$ is a dicotyledonous species [13]. AYB is an important food crop in tropical Africa with great medicinal values and pesticidal potential [14]. AYB contains approximately 29 and 19% crude protein in its grain and tuber, respectively, though lower than that of soybean (38%) [15]. The seeds are edible like the common beans and cowpea (*Vigna unguiculata*), and the tubers are richer in protein than Irish potatoes and 10 times the amount in cassava tubers [16, 17]. The whole seed is also rich in potassium (649.49 mg/100 g) and phosphorus (241.21 mg/100 g) [16]. The most prominent minerals in AYB whole seeds were reported as magnesium (454.16 mg/100 g), potassium (398.25 mg/100 g), and phosphorous (204.86 mg/100 g) with appreciable amounts of calcium (37.44 mg/100 g) and iron (11.70 mg/100 g) [18]. Similarly, Ojuederie and Balogun [18] confirmed the average proximate parameters of AYB seeds to include protein (22.40%), fat (1.90%), total carbohydrate (56.40%), total ash (3.60%), and moisture (11.80%) with a caloric value of 1396.10 KJg^{-1} . Some of the accessions evaluated in their study had up to 25% protein (TSs 41, TSs150, and TSs152). An inverse relationship was detected between the concentrations of protein and carbohydrate. Higher carbohydrate content of 62.50% was obtained in accession TSs153, with a protein content of 19.30% [18]. The pods and seeds are resistant to major pests of cowpea such as cowpea pod borer (*Maruca vitrata*) and cowpea weevil (*Callosobruchus maculatus*) [19, 20]. This resistance was attributed to the lectin present in the seeds as confirmed in the study of Ojuederie [21] who reported high levels of lectin in the seeds of AYB especially for accessions TSs68 (73.34 Lu mg^{-1}) and TSs5 (66.87 Lu mg^{-1}). Valuable diversities that can be explored for diverse utilization purposes have also been reported in AYB [9, 22, 23].

3.1.2 Bambara groundnut (*Vigna subterranea*)

Bambara groundnut (*Vigna subterranea*) is less used in many parts of Africa, yet its nutritional and health benefits are well established [24]. It is the fourth crop among the grain legume crops after the well-known groundnut, cowpea, and soybean. In recent times, there has been renewed interest for cultivation of *V. subterranea* in the arid savannah zones to mitigate the effect of stress and increase protein supply to people of that region [24]. Bambara groundnut is resistant to drought, withstands stress, contains higher nutrients than other legumes, and is known to produce good yield even when grown on poor soils [25]. The protein composition contains 6–43% globulin, 14–71% albumin, 1.6–2.2% prolamins, and 3.3–5.2% glutelins [26]. Bambara groundnut gets about 51–67% of their N nutrition from symbiotic fixation; hence the crop could serve as high-protein forage for livestock [24, 26].

3.1.3 Winged bean (*Psophocarpus tetragonolobus*)

Psophocarpus tetragonolobus popularly known as winged bean with somatic chromosome number of $2n = 18$ is one of the old legumes [27]. Winged bean is a multipurpose legume plant with all parts being edible and useful as medicine in tropics of Asia, Africa, and Latin America. It is grown in many parts of the humid tropics, including Central and South America, the Caribbean, Africa, Oceania, and Asia [28]. All parts of the plant are considered rich in vitamins, minerals, protein, and secondary metabolites such as phenolic and flavonoids [28]. Leaves are usually eaten like spinach, flowers are used in salads, tubers are eaten raw or cooked, while

seeds are consumed when cooked [29]. In addition, winged bean is highly resistant to biotic and abiotic stresses and thus capable of growing under varying environmental conditions. It is now a toast of many scientists trying to explore its rich potentials [28, 30]. The seeds of winged bean also exhibit tolerance to storage pests [31]. Apart from its seeds, the tubers/roots are also nutritious and rich in protein of about 20%, while the leaves and flowers are also high in protein (10–15%) [32].

3.1.4 Lima bean (*Phaseolus lunatus* L.)

Lima bean is grown for its edible seeds and as leafy vegetable in the Caribbean, Peru, Mexico, and Asian regions [33, 34]. Rich in protein, lima beans are resistant to viral and rust diseases and withstand insect pests, drought, and abiotic stress [35]. The species also tolerates different levels of aluminum and manganese toxicity which can be exploited to advance the sustainable utilization of other legumes [36].

3.1.5 Hyacinth bean (*Lablab purpureus* L.)

Hyacinth bean (*Lablab purpureus* L.) is cultivated for its edible seeds and pods. It is mainly grown in Africa and Asia as source of food in the form of vegetable, green pods, and seeds [37]. Several field trials suggested that the species is drought tolerant and water efficient and produces high yield [37, 38]. The protein content is comparable to that of soybean. Reports also indicate that *L. purpureus* has potential to be a source of pharmaceuticals and nutraceutical as medicine and traditional medicine in Asia and Africa [37].

3.1.6 Jack bean (*Canavalia ensiformis* L.)

Canavalia ensiformis known as jack bean is the most economically important species in the genus *Canavalia*, with enormous potentials to serve as food for both humans and livestock [39]. It is widely distributed in Africa, Asia, and America, with large-scale cultivation reported in Congo and Angola [39]. It is rich in protein and thrives well in poor and acidic soils. Jack bean is mainly grown for its nutritious pods, seeds, and as fodder. It is a forage crop with high green manure capacity to enrich the soils and also to control soil erosion. The crop tolerates adverse environment, drought, heat, and leached soils; also it resists pest attacks [40]. The leaf of jack bean contains crude proteins and fiber comparable to other legumes [15, 39, 40]. Jack bean possesses deep root system which enables the plant to penetrate deeply into the soil which enables it to withstand very dry conditions. Raw jack bean contains toxic compounds such as tannin, phytate, saponins, canavanine, concaavalin A (hemagglutinin), and trypsin inhibitors [40].

3.1.7 Sword bean (*Canavalia gladiata* L.)

Sword bean (*Canavalia gladiata* L.) is another species in the genus *Canavalia* of the Fabaceae family with rich potentials likely to be adopted as an important source of food, leafy vegetable, medicine, forage, and as cover crop. It is a vigorous perennial climber plant usually cultivated as an annual. Reports indicated that sword bean originated from the Asian continent and is now known in the tropics as an introduced species. The red sword bean is one of the edible beans of China reportedly rich in antioxidant polyphenols with great medicinal uses [41, 42]. Furthermore, the seed coat of the bean is rich in gallic acid and its derivatives, mainly gallotannins, a common trait found in legume polyphenols [41]. The chemical composition of seeds of sword bean has been reported and compares quite well

with soybean [43–45]. Average yield ranges from 720 to 1500 kg/ha which can be compared with soybean yield of 600–1000 kg/ha [43, 46]. The fruits mature in 6–10 months after planting. The sword bean is relatively resistant to attack from pests and diseases [43].

3.1.8 Pigeon pea (*Cajanus cajan* L. Millsp)

Cajanus cajan, commonly known as pigeon pea, is an erect, perennial shrub, or woody plant widely grown in the tropical regions [47]. Pigeon pea is mainly cultivated for its edible seed grains as well as feed, forage, and fuel. It has a diploid genome with somatic chromosome number of $2n = 22$ [47]. Most farmers depend on *C. cajan* as alternative source of protein to support workers and families during lean times [47]. The plant grows well in areas with low rainfall and varying climatic conditions. It is a drought-tolerant crop capable of withstanding poor soil and abiotic stress [48]. Diversity exists in seed coat color, size, texture, and taste. The leaves are source of medicine in combination with other plants such as mango and lemon to treat malaria and typhoid fever. The dried woody stem is used as firewood for cooking by women in farms. Its seed protein content is high (20–22%) and is quite rich in vitamins such as vitamin B and minerals which can promote health [47].

3.1.9 Kersting's groundnut (*Kerstingiella geocarpa* Harms)

Kersting's groundnut is an indigenous legume grown in Africa for its edible seeds. It is considered rich in nutritional proteins and minerals. Its protein content of 12.9% is higher than that of bambara groundnut (12.1%) and cowpea (7.1%), while the total amino acid content of the seed is 42% [49]. It is a likely alternative source of quality protein for feed and food in the tropics [50, 51]. The crop can withstand drought, pest, and diseases. It adapts to varying ecological conditions of tropical Africa. However, only the elderly farmers cultivate this crop as alternative source of protein, and as such it has been neglected and underutilized in several African countries.

3.2 Research efforts and constraints to the global cultivation and adoption of MNUGLs

MNUGLs are increasingly becoming rare across the world with their associated valuable genetic resources disappearing rapidly in all their natural ranges. Therefore, there is the need for a paradigm shift from present scenario of neglect to sustainable cultivation, exploitation, and utilization of the species. In recent years, grain legume stakeholders had advocated for an increased global cultivation and production of MNUGLs toward sustainable solution to food and protein security, plus agricultural and environmental restoration [1, 52]. Similarly, significant efforts are ongoing to increase genomic resources and apply innovative breeding techniques to improve the nutritional quality and yield of legume crops, alongside enhanced resilience to climate change [1, 53]. MNUGLs are highly adapted to agroecological niches/marginal areas having capacity to contribute considerably to global protein security and productive agricultural practices and alleviate rural poverty, among others. The potential genetic resources available among and within the MNUGLs have not been properly explored to advance sustainable utilization for future food and nutritional security as well as biodiversity maintenance to alleviate the negative effects of climate change and abiotic stress. Likewise, the possibilities of the species to withstand abiotic stress even in the face of biological limiting factors are important to their continued use and survival. In order to prevent total

genetic erosion/loss of valuable genetic resources and exploit MNUGLs for present and future food, nutrition, and protein security, a holistic approach needs to be adopted to improve the species.

Constraints limiting the sustainable cultivation and utilization of MNUGLs include long cooking time of seeds, growth habit requiring mandatory staking, intensive labor requirements, and lack of staking materials [22, 54, 55]. Others are low product market demand, poor seed quality, high cost of labor, postharvest diseases, and anti-nutritional factors (ANF) [55]. The constraints to cultivation and utilization of MNUGLs, breeding intervention approaches, and possible solutions are presented in **Table 1**.

3.3 Genetic potentials of MNUGLs

In recent times, the Food and Agriculture Organization (FAO) of the United Nations estimated that around 800 million people particularly in the developing countries suffer from food and nutrition insecurity [82]. The Sustainable Development Goals (SDGs) of the 2030 Agenda adopted by the United Nations in September 2015 (<https://sustainabledevelopment.un.org/>) also aimed at having zero hunger as one of its SDGs by abolishing hunger and malnutrition especially in the less developed world (<https://sustainabledevelopment.un.org/sdg2>). A tactical approach to addressing this challenge is to promote biodiversity and utilization of the neglected and underutilized crop species in the dietary and food pattern of the people [5, 82, 83]. The MNUGLs could increase food production levels, diversify the human diet, and enhance sustainable utilization of broad spectrum of climate smart crops [6, 82, 84]. Additionally, MNUGLs are rich in nutrients and health-enhancing composites that are capable of preventing malnutrition and some chronic diseases [1, 52, 55, 82]. Awareness programs in local communities around the world on the rich potentials of MNUGLs and their inclusion in local diets could also be an effective tool to improve human nutrition and health. MNUGLs could be exploited to achieve optimum utilization to meet human nutritional needs in the developing world.

Though huge genetic potentials exist among and within MNUGLs, genetic erosion or loss of valuable genetic resources is alarming. The discovery and utilization of untapped potential genetic resources within the minor crop gene pool deserve research attention. Concerted research efforts are therefore needed to prevent the continuous loss of genetic resources among the MNUGLs. Recent reports indicate that development of effective phenotyping and breeding approaches constitute a challenge among the MNUGLs [1]. Modern breeding efforts to improve disease resistance, quality, and yield are also constrained by low level of genetic diversity available to breeding programs [1, 52]. Though fairly large genetic diversity exists in seeds of grain legumes in gene banks, such diversities have not been fully utilized in active breeding programs [1, 85, 86]. Large quantities of these minor grain legumes are reportedly available in Africa [87] which if properly harnessed could mitigate the effect of malnutrition and poverty in sub-Saharan Africa. The diversity existing among the seeds of the species are worthy of research attention for food, agriculture, and medicine (**Figure 1**).

3.4 Genetic improvement and prospects of MNUGL

Genetic and breeding efforts to improve the underutilized and neglected legume crops in architecture, period of maturation, yield, and nutritional contents have not recorded commiserate level of success as expected [88, 89]. Traditional hybridization and other breeding techniques, though have been used for some desired

Species	Common name	Constraints	Breeding intervention approaches	Possible solutions	References
<i>Sphenostylis stenocarpa</i>	African yam bean (AYB)	Long cooking time of seeds, growth habit requiring mandatory staking, low product market demand, poor seed quality, high cost of labor, postharvest diseases, pod shattering, and anti-nutritional factors (ANF)	Traditional breeding approach, assessment of genetic diversity of landraces using molecular markers (AFLP, SSR), and marker-assisted selection. No successful breeding lines so far	Tissue culture, micropropagation, morphological evaluation of AYB for desirable agronomic traits and for breeding purposes. Whole genome sequencing and the use of gene editing tools to improve the species genetically on the observed constraints	[9, 12, 21, 56–58]
<i>Vigna subterranea</i>	Bambara groundnut	Labor intensive, low seed supply to farmers, pest attack, low yield, long cooking time, anti-nutritional factors, and difficulty in dehulling	Assessment of genetic diversity of landraces using SSR marker	Mutation breeding for genetic enhancement of protein and methionine contents, effective processing methods, mapping and QTL analysis of phenotypic traits in F2 and F3 derived genotypes, whole genome sequencing, and the use of gene editing tools to improve the species genetically on the observed constraints	[32, 59, 60–64]
<i>Psophocarpus tetragonolobus</i>	Winged bean	Indeterminate growth habit, high cost of labor, ANF, pod shattering, late maturing, low yield, and scandent habit	Use of molecular genetic tools to support genetic improvement, gene-based SSR markers, mutation breeding to obtain varieties with erect stem, multiple branches, bushy habit, and long pods	Transcriptome sequencing for gene discovery and marker development. Comparative genomic analyses coupled with NGS sequencing, identification of functional SNPs associated with agronomically important traits, and the use of gene editing tools to improve the species	[32, 65–67]
<i>Phaseolus lunatus</i>	Lima bean	Pest and disease attacks, market constraints, growth habit requiring mandatory staking	Transcriptome sequencing to identify and select putative parents/hybrid for genetic improvement	Transcriptome sequencing for gene discovery and development of marker, early maturing, dwarf, erect, high yielding, and non-shattering varieties with reduced anti-nutritional factors	[68]
<i>Lablab purpureus</i>	Dolichos/hyacinth bean	Pest and disease attacks	Molecular characterization using SSR markers for classifying dolichos bean based on photoperiod sensitivity	Development of expressed sequence tags (ESTs) and transferability of SSR markers from other legumes for diversity evaluation, applications of metabolomics, proteomics and next-generation sequencing technologies to discover candidate markers for the development of agronomically improved varieties	[69–73]

Species	Common name	Constraints	Breeding intervention approaches	Possible solutions	References
<i>Canavalia ensiformis</i>	Jack bean	Long cooking period, intensive labor requirements, low economic gain, and anti-nutritional factors	Little or no breeding intervention approaches	Breeding for host plant resistance and general genetic improvement	[74, 75]
<i>Canavalia gladiata</i>	Sword bean	Hard seed coat, insect pest attack, anti-nutritional factors	Little or no breeding intervention approaches	Breeding for host plant resistance and general genetic improvement	[74, 75]
<i>Cajanus cajan</i>	Pigeon pea	Tall, shrubby, and woody habit, insect pest attack, long cooking period, and intensive labor requirement	Genetic diversities evaluated using AFLP, DarT, SSR, and SNPs, development of new hypervariable SSR markers, ESTs characterized, and transcriptome sequencing to characterize putative hybrids	More development of genomic resources, transcript profiling in combination with genome editing tools to identify expression quantitative loci (eQTLs), and general genetic improvement of the species	[76–78]
<i>Kerstingiella geocarpa</i>	Kersting's groundnut	Postharvest pest attack	Little or no breeding intervention approaches	Breeding for host plant resistance and general genetic improvement	
<i>Phaseolus vulgaris</i>	Common bean	Pest and disease attacks, rarity of improved germplasm, poor marketing value, low yield, and susceptibility to harsh climatic conditions	Breeding, screening, evaluation, and comparison of the genetic potentials of hybrids for improved grain yield using best and suitable methods on segregating populations	Development of drought-tolerant varieties and water use efficiency, breeding for improved cooking time, and the use of genotyping by sequencing for rapid identification of large number of SNPs for trait mapping	[79–81]

Table 1. Cultivation constraints, breeding intervention approaches, and possible solutions for some underutilized legumes.



Figure 1.

Some selected underutilized and neglected legumes showing diversity in their seeds. (A) African yam bean (*Sphenostylis stenocarpa* Ex. A. Rich Harms). (B) Sword bean (*Canavalia gladiata* L.). (C) Jack bean (*Canavalia ensiformis* L.). (D) Hyacinth bean (*Lablab purpureus* L.). (E) Bambara groundnut (*Vigna subterranean* L. Verdc.). (F) Lima bean (*Phaseolus lunatus* L.). Source of seeds: Genetic Resources Centre of the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria.

intentions, are yet to translate to desired results. Few successful crosses have been recorded so far on MNUGLs. Few successes have been reported on *Cajanus cajan* and some species [90, 91]. Reproductive barriers such as embryo abortion have been reported in many MNUGLs as limiting factors to genetic enhancement/improvement. However, tissue culture and micropropagation could be further employed to overcome such barriers with capacity to generate fertile haploid plants [5, 6].

Advancement in DNA technology has enhanced our understanding on the huge potentials available in the genome of many plant species and particularly the underutilized legumes. Several genomic breakthroughs involving genetic engineering of cereal crops have been reported [92, 93]. DNA-based methods are reliable and have been employed to identify, trace, and certify plant genealogies, origins, and phylogenetic relationships [94, 95]. DNA barcoding has been applied to identify and characterize some underutilized and neglected legumes such as *Lablab purpureus*, *Tylosema esculentum*, *Vigna subterranea*, *V. vexillata*, and *Vigna unguiculata* [96, 97].

The use of molecular markers for marker-assisted selection (MAS) or breeding programs has played significant roles in the assessment of the level of genetic diversity or relatedness among various species of underutilized legumes [9, 98]. Globally, different DNA techniques such as random amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLPs), inter simple sequence repeats (ISSR), single feature polymorphisms (SFP), single-nucleotide polymorphisms (SNP), and chloroplast gene RBCL, among others, have been employed to evaluate the genetic relationships and diversities among neglected underutilized species [85, 99, 100]. RAPD and ISSR markers were used for genetic diversity studies in winged bean by Mohanty et al. [101]. The study linked the physiological and phytochemical parameters to the genotypes investigated. Distinct winged bean novel lines were identified, and the information from analysis of photosynthesis

rate, photosynthetic yield, and stomatal conductance data revealed two clusters in correspondence with the phytochemical affinities of the genotypes. The use of SSR, SNP, and genotype by sequencing (GBS) for the studies of phylogenetic relationships and genetic diversities among the MNUGLs is rare due to lack of sequence information; hence RAPD and AFLP were used for such species, and attempts were made in transferability of specific SSR markers in cowpea for genetic diversity studies in underutilized legumes by other authors as in the case of African yam bean [12].

Globally, complexity of plant genomes had led to advancement in genome sequencing, determination of polyploidy, genome size, repetitive DNA sequences, and transposable elements toward genetic engineering of plants to generate useful products apart from innate uses [102, 103]. Transposable elements (TEs) are ubiquitous in flowering plant genomes of which higher percentage of such genomes are occupied by TEs [104]. Studies have shown that TEs via their amplification, methylation, and recombination contribute to the restructuring of plant genomes, epigenomes, centromeric regions, and evolution of new genes for novel genetic functions [99, 105, 106]. Identification of TEs in a species is critically significant to the understanding of their functional roles [107]. Therefore, detail description of TEs is a major procedure to precisely identify specific genes and evaluate association between genes and TEs in a complex sequenced genome [107]. Such studies have not been applied on MNUGLs to understand the role of transposons in long duration of seed cooking of most of the MNUGLs and expressivity of secondary nutritional metabolites. We believe that such studies will have an overall influence on the genetic manipulation of the MNUGLs, understanding of potential gene-TE interaction, identification of active TEs for functional genomics, and development of TE-based molecular markers for genotyping studies. Currently, sophisticated sequencing genomic approaches such as de novo transcriptome sequencing are being utilized to identify and describe key genes responsible for varied economic, nutritional, physiological, and pharmaceutical uses of plant species [30, 88, 108, 109]. Transcriptome sequence analysis is one of the molecular tools that can also be applied to MNUGLs for improvement purposes. It is hoped that some of these tools will be employed in due course, not only to analyze genetic diversity among the MNUGLs but also to identify key genes that will be potentially useful for breeding and utilization purposes. Genes that are useful for varied needs could be identified, described, and extracted from the MNUGLs, thus ensuring the sustainable utilization of the species. Proteomics and genomics are increasingly being applied to unravel a number of genetic constraints and proffer robust solutions toward their sustainable production and utilization [24, 110]. These areas combined with metabolomics offers great possibility in the quest for improvement of MNUGLs. Consequently, the application of molecular breeding tools such as marker-assisted selection, genomic selection (GS), and genome-wide association (GWAS) has been appraised to influence scientific efforts for improving grain yield of orphan crops in the developing countries [111, 112]. These of course, including next-generation sequencing (NGS), have greatly enhanced the improvement of many commercial crops which the MNUGLs can also benefit from.

Recent advancement in omic technologies such as genomics, proteomics, transcriptomics, and metabolomics has equally enhanced our understanding of the genetic structure of plant species, as well as the expression of genes through transcriptomic/proteomic profiling and their role in the overall metabolism of plants [32, 113]. Recently Vatanparast et al. [32] used transcriptome sequencing to develop SSR and SNP markers for winged bean (*Psophocarpus tetragonolobus*) and also gave insights into the divergence of the Kunitz-type trypsin inhibitors, which are essential anti-nutritional factors in winged bean and other legumes. Transcriptome

sequencing is inexpensive and a reliable method for efficient and rapid identification of molecular markers in underutilized plant species [32]. Future prospects also lie in the adoption of high-throughput tools including gene editing, GWAS, and clustered regularly interspaced short palindromic repeat (CRISPR), among others, toward genetic improvement of the species for sustainable cultivation, production, and utilization.

4. Conclusions

Significant improvement and scientific breakthroughs have been reported on many crop species based on molecular characterization, linkage genetic maps, MAS, and genomics, which cannot be said of MNUGLs [114, 115]. MAS in combination with the traditional hybridization techniques provides clear-cut potential to enhance the overall improvement of plant species. The areas of genomics and proteomics are rapidly expanding in the field of food and agriculture, medicine, and environment. Though few genomic studies have been conducted on some MNUGLs, proteomics and metabolomics have not been employed to explore the rich potentials available in MNUGLs. Generally, these sets of grain legumes have not been subjected to biotechnological techniques/solutions including sophisticated tissue culture micropropagation and genetic engineering which offer great opportunities to improve the species for sustainable utilization. Genome editing provides the possibility to modify the genomes of the MNUGLs particularly for plant architecture, hardness of the seeds, and anti-nutritional factors. The emergence of the CRISPR technology supports this position to possibly enhance the genomes of MNUGLs for higher productivity and utilization via removal of the constraints. Added to this advancement is the use of high-throughput targeted genotyping using next-generation sequencing to effectively unravel the rich diversity potentials available among the MNUGLs. Through proteomic analysis, essential genes and their pathways can be discovered. This is of utmost importance considering the present increased changes in climatic conditions leading to abiotic stresses such as drought and extreme temperatures. MNUGLs are known to be resilient crops capable of withstanding unfavorable environmental conditions. Proteomics therefore offers plant breeders the opportunity to study the broad spectrum of proteins present in underutilized plant species and could give a clue on specific proteins produced by MNUGLs under abiotic stresses, as well as information relating to nutritional and yield traits. On global research funds and activities, research funds are usually not available for these species as many funding agencies or organizations are skeptical about their sustainable utilization and overall benefits to human and environment and hence to the organizations. Stakeholders including policy-makers and plant breeders, among others, should as a matter of urgent priority consider the MNUGLs as important crops for research and development toward food and nutritional security as well as socioeconomic development of rural areas where these species are abundantly available.

Conflict of interest

Authors declare no conflict of interests.

IntechOpen

Author details

Jacob Popoola^{1*}, Omena Ojuederie², Conrad Omonhinmin¹ and Adegoke Adegbite³

¹ Biotechnology Cluster Group, Department of Biological Sciences, College of Science and Technology, Covenant University, Ota, Ogun State, Nigeria

² Food Security and Safety Niche Area, Faculty of Natural and Agricultural Sciences, North West University, Mafikeng Campus, Mafikeng, South Africa

³ Department of Biological Sciences, Ondo State University of Science and Technology, Okitipupa, Nigeria

*Address all correspondence to: jacob.popoola@covenantuniversity.edu.ng

IntechOpen

© 2019 The Author(s). Licensee IntechOpen. This chapter is distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/3.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. 

References

- [1] Considine MJ, Siddique KHM, Foyer CH. Nature's pulse power: Legumes, food security and climate change. *Journal of Experimental Botany*. 2017;**68**(8):1815-1818. PubMed PMID: 28499041. PMCID: PMC5429020. Epub 2017/05/13. eng
- [2] Padulosi S, Thompson J, Rudebjer P. Fighting Poverty, Hunger and Malnutrition with Neglected and Underutilized Species: Needs, Challenges and the Way Forward. Rome, Italy: Bioversity International; 2013
- [3] Singh RJ, Chung GH, Nelson RL. Landmark research in legumes. *Genome*. 2007;**50**(6):525-537. PubMed PMID: 17632574. Epub 2007/07/17. eng
- [4] Li Y, Ruperao P, Batley J, Edwards D, Khan T, Colmer TD, et al. Investigating drought tolerance in chickpea using genome-wide association mapping and genomic selection based on whole-genome resequencing data. *Frontiers in Plant Science*. 2018;**9**:190
- [5] Cullis C, Kunert KJ. Unlocking the potential of orphan legumes. *Journal of Experimental Botany*. 2017;**68**(8):1895-1903. PubMed PMID: 28003311. Epub 2016/12/23. eng
- [6] Mabhaudhi T, Chimonyo VGP, Chibarabada TP, Modi AT. Developing a roadmap for improving neglected and underutilized crops: A case study of South Africa. *Frontiers in Plant Science*. 2017;**8**:2143. PubMed PMID: 29312397. PMCID: PMC5735103. Epub 2018/01/10. eng
- [7] Hnatuszko-Konka K, Kowalczyk T, Gerszberg A, Wiktoerek-Smagur A, Kononowicz AK. *Phaseolus vulgaris*—recalcitrant potential. *Biotechnology Advances*. 2014;**32**(7):1205-1215. PubMed PMID: 24953179. Epub 2014/06/24. eng
- [8] Popoola JO, Adebambo A, Ejoh AS, Agre P, Adegbite AE, Omonhinmin CA. Morphological diversity and cytological studies in some accessions of *Vigna vexillata* (L.) A. Richard. *Annual Research and Review in Biology*. 2017;**19**(5):1-12
- [9] Ojuederie OB, Balogun MO, Fawole I, Igwe DO, Olowolafe MO. Assessment of the genetic diversity of African yam bean (*Sphenostylis stenocarpa* Hochst ex. A Rich. Harms) accessions using amplified fragment length polymorphism (AFLP) markers. *African Journal of Biotechnology*. 2014;**13**(18):1850-1858
- [10] Ofosu IW, Ellis WO, Nsiah K, Oduro IN. Neglected and underutilized legumes (NULs) hazards and probabilistic risks associated with some selected dietary lectins. *Journal of Food Security*. 2017;**5**(6):212-222
- [11] Omonhinmin CA, Ogunbodede OO. Genetic diversity, taxonomy and legumins implications of seed storage protein profiling in Fabaceae. *African Journal of Biotechnology*. 2013;**12**(17):36-42
- [12] Shitta NS, Abberton MT, Adesoye AI, Adewale DB, Oyatomi O. Analysis of genetic diversity of African yam bean using SSR markers derived from cowpea. *Plant Genetic Resources*. 2016;**14**(1):50-56
- [13] Popoola JO, Obembe OO, Adegbite AE. Cytological studies on some accessions of African yam bean (AYB) (*Sphenostylis stenocarpa* Hochst. Ex. A. Rich. Harms). *International Research Journal of Plant Science*. 2011;**2**(8):249-253
- [14] Machuka JS, Okeola OG, Chrispeels MJ, Jackai LE. The African yam bean seed lectin affects the development of the cowpea weevil

but does not affect the development of larvae of the legume pod borer. *Phytochemistry*. 2000;**53**(6):667-674. PubMed PMID: 10746879. Epub 2000/04/04. eng

[15] Oboh HA, Muzquiz M, Burbano C, Cuadrado C, Pedrosa MM, Ayet G, et al. Anti-nutritional constituents of six underutilized legumes grown in Nigeria. *Journal of Chromatography. A*. 1998;**823**(1-2):307-312. PubMed PMID: 9818409. Epub 1998/11/18. eng

[16] Oshodi AA, Ipinmoroti KO, Adeyeye EI. Functional properties of some varieties of African yam bean (*Sphenostylis stenocarpa*) flour-III. *International Journal of Food Sciences and Nutrition*. 1997;**48**(4):243-250. PubMed PMID: 9349440. Epub 1997/07/01. eng

[17] Onyeike EN, Omubo-Dede TT. Effect of heat treatment on the proximate composition, energy values, and levels of some toxicants in African yam bean (*Sphenostylis stenocarpa*) seed varieties. *Plant Foods for Human Nutrition* (Dordrecht, Netherlands). 2002;**57**(3-4):223-231. PubMed PMID: 12602931. Epub 2003/02/27. eng

[18] Ojuederie OB, Balogun MO. Genetic variation in nutritional properties of African yam bean *Sphenostylis stenocarpus* (Hochst ex. A. Rich. Harms) accessions. *Nigerian Journal of Agriculture, Food and Environment*. 2017;**13**(1):180-187

[19] Machuka J, Okeola OG. One- and two-dimensional gel electrophoretic identification of African yam bean seed proteins. *Journal of Agricultural and Food Chemistry*. 2000;**48**(6):2296-2299. PubMed PMID: 10888540. Epub 2000/07/11. eng

[20] Okeola OG, Machuka J. Biological effects of African yam bean lectins on *Clavigralla tomentosicollis* (Hemiptera: Coreidae). *Journal of Economic Entomology*. 2001;**94**(3):724-729.

PubMed PMID: 11425030. Epub 2001/06/27. eng

[21] Ojuederie O, Balogun M, Abberton M. Mechanism for pollination in African yam bean. *African Crop Science Journal*. 2016;**24**(4):405-416

[22] Popoola J, Adegbite A, Obembe O, Adewale B, Odu B. Morphological intraspecific variabilities in African yam bean (AYB) (*Sphenostylis stenocarpa* ex. A. Rich) Harms. *Scientific Research and Essays*. 2011;**6**(3):507-515

[23] Adewale B, Kehinde O, Aremu C, Popoola J, Dumet D. Seed metrics for genetic and shape determinations in African yam bean [Fabaceae] (*Sphenostylis stenocarpa* Hochst. Ex. A. Rich.) harms. *African Journal of Plant Science*. 2010;**4**(4):107-115

[24] Aliyu S, Massawe F, Mayes S. Beyond landraces: Developing improved germplasm resources for underutilized species—A case for Bambara groundnut. *Biotechnology and Genetic Engineering Reviews*. 2014;**30**(1-2):127-141. PubMed PMID: 25603880. Epub 2015/01/22. eng

[25] Chibarabada TP, Modi AT, Mabhaudhi T. Nutrient content and nutritional water productivity of selected grain legumes in response to production environment. *International Journal of Environmental Research and Public Health*. 2017;**14**(11):1-17. PubMed PMID: 29072620. PMCID: PMC5707939. Epub 2017/10/27. eng

[26] Hillocks R, Bennett C, Mponda O. Bambara nut: A review of utilisation, market potential and crop improvement. *African Crop Science Journal*. 2012;**20**(1):1-16

[27] Bottino P, Maire C, Goff L. Tissue culture and organogenesis in the winged bean. *Canadian Journal of Botany*. 1979;**57**(17):1773-1776

- [28] Yang S, Grall A, Chapman MA. Origin and diversification of winged bean (*Psophocarpus tetragonolobus* (L.) DC.), a multipurpose underutilized legume. *American Journal of Botany*. 2018;**105**(5):888-897. PubMed PMID: 29874397. Epub 2018/06/07. eng
- [29] Amoo I, Adebayo O, Oyeleye A. Chemical evaluation of winged beans (*Psophocarpus tetragonolobus*), Pitanga cherries (*Eugenia uniflora*) and orchid fruit (Orchid fruit myristic a). *African Journal of Food, Agriculture, Nutrition and Development*. 2006;**6**(2):1-12
- [30] Singh V, Goel R, Pande V, Asif MH, Mohanty CS. De novo sequencing and comparative analysis of leaf transcriptomes of diverse condensed tannin-containing lines of underutilized *Psophocarpus tetragonolobus* (L.) DC. *Scientific Reports*. 2017;**7**:44733. PubMed PMID: 28322296. PMCID: PMC5359716. Epub 2017/03/23. eng
- [31] Wong Q, Massawe F, Mayes S. Improving winged bean (*Psophocarpus tetragonolobus*) productivity: An analysis of the determinants of productivity. *Acta Horticulturae*. 2015;**1102**:83-88
- [32] Vatanparast M, Shetty P, Chopra R, Doyle JJ, Sathyanarayana N, Egan AN. Transcriptome sequencing and marker development in winged bean (*Psophocarpus tetragonolobus*; Leguminosae). *Scientific Reports*. 2016;**6**:29070
- [33] Andueza-Noh RH, Martinez-Castillo J, Chacon-Sanchez MI. Domestication of small-seeded lima bean (*Phaseolus lunatus* L.) landraces in Mesoamerica: Evidence from microsatellite markers. *Genetica*. 2015;**143**(6):657-669. PubMed PMID: 26391600. Epub 2015/09/24. eng
- [34] Sprent JJ, Odee DW, Dakora FD. African legumes: A vital but under-utilized resource. *Journal of Experimental Botany*. 2010;**61**(5):1257-1265. PubMed PMID: 19939887. Epub 2009/11/27. eng
- [35] Ballhorn DJ, Kautz S, Heil M, Hegeman AD. Cyanogenesis of wild lima bean (*Phaseolus lunatus* L.) is an efficient direct defence in nature. *PLoS One*. 2009;**4**(5):e5450. PubMed PMID: 19424497. PMCID: PMC2675055. Epub 2009/05/09. eng
- [36] Azeke MA, Elsanhoty RM, Egielewa SJ, Eigbogbo MU. The effect of germination on the phytase activity, phytate and total phosphorus contents of some Nigerian-grown grain legumes. *Journal of the Science of Food and Agriculture*. 2011;**91**(1):75-79. PubMed PMID: 20859988. Epub 2010/09/23. eng
- [37] Morris JB. Morphological and reproductive characterization in hyacinth bean, *Lablab purpureus* (L.) sweet germplasm with clinically proven nutraceutical and pharmaceutical traits for use as a medicinal food. *Journal of Dietary Supplements*. 2009;**6**(3):263-279. PubMed PMID: 22435478. Epub 2009/01/01. eng
- [38] Vidigal P, Duarte B, Cavaco AR, Cacador I, Figueiredo A, Matos AR, et al. Preliminary diversity assessment of an undervalued tropical bean (*Lablab purpureus* (L.) Sweet) through fatty acid profiling. *Plant Physiology and Biochemistry*. 2018;**132**:508-514. PubMed PMID: 30308461. Epub 2018/10/12. eng
- [39] Akpapunam M, Sefa-Dedeh S. Jack bean (*Canavalia ensiformis*): Nutrition related aspects and needed nutrition research. *Plant Foods for Human Nutrition*. 1997;**50**(2):93-99
- [40] Sivaraj N, Sunil N, Pandravada S, Kamala V, Rao B, Prasad R, et al. Fatty acid composition in seeds of Jack-bean [*Canavalia ensiformis* (L.) DC.] and Sword-bean [*Canavalia gladiata* (Jacq.) DC.] Germplasm from South India:

A DIVA-GIS analysis. Seed Technology. 2010;**32**(1):46-53

[41] Gan RY, Kong KW, Li HB, Wu K, Ge YY, Chan CL, et al. Separation, identification, and bioactivities of the main galloytannins of red sword bean (*Canavalia gladiata*) Coats. Frontiers in Chemistry. 2018;**6**:39. PubMed PMID: 29541634. PMCID: PMC5835520. Epub 2018/03/16. eng

[42] Ekanayake S, Jansz ER, Nair BM. Literature review of an underutilized legume: *Canavalia gladiata* L. Plant Foods for Human Nutrition (Dordrecht, Netherlands). 2000;**55**(4):305-321. PubMed PMID: 11086874. Epub 2000/11/22. eng

[43] Ekanayake S, Nair B, Jansz ER, Asp NG. Effect of processing on the protein nutritional value of *Canavalia gladiata* seeds. Die Nahrung. 2003;**47**(4):256-260. PubMed PMID: 13678265. Epub 2003/09/19. eng

[44] Eknayake S, Jansz ER, Nair BM. Proximate composition, mineral and amino acid content of mature *Canavalia gladiata* seeds. Food Chemistry. 1999;**66**(1):115-119

[45] Ekanayake S, Skog K, Asp N-G. Canavanine content in sword beans (*Canavalia gladiata*): Analysis and effect of processing. Food and Chemical Toxicology. 2007;**45**(5):797-803

[46] Sharma KK, Sreelatha G, Dayal S. Pigeonpea (*Cajanus cajan* L. Millsp.). Methods in Molecular Biology (Clifton, NJ). 2006;**343**:359-367. PubMed PMID: 16988359. Epub 2006/09/22. eng

[47] Munoz N, Liu A, Kan L, Li MW, Lam HM. Potential uses of wild germplasms of grain legumes for crop improvement. International Journal of Molecular Sciences. 2017;**18**(2):1-28. PubMed PMID: 28165413. PMCID: PMC5343864. Epub 2017/02/07. eng

[48] Ajayi OB, Oyetayo FL. Potentials of *Kerstingiella geocarpa* as a health food. Journal of Medicinal Food. 2009;**12**(1):184-187. PubMed PMID: 19298213. Epub 2009/03/21. eng

[49] Obasi M, Agbatse A. Evaluation of nutritive value and some functional properties of Kersting's groundnut, (*Kerstingiella geocarpa* harms). Seeds for optimal utilization as food and feed source. The East African Agricultural Journal. 1994;**54**:66-74

[50] Obasi M, Ezedinma F. Floral biology of Kerstings groundnut (*Kerstingiella geocarpa* Harms). Ghana Journal of Agricultural Science. 1991;**24-27**:145-149

[51] Foyer CH, Lam HM, Nguyen HT, Siddique KH, Varshney RK, Colmer TD, et al. Neglecting legumes has compromised human health and sustainable food production. Nature Plants. 2016;**2**:16112. PubMed PMID: 28221372. Epub 2017/02/22. eng

[52] Foyer CH, Siddique KHM, Tai APK, Anders S, Fodor N, Wong FL, et al. Modelling predicts that soybean is poised to dominate crop production across Africa. Plant, Cell and Environment. 2019;**42**(1):373-385. PubMed PMID: 30329164. Epub 2018/10/18. eng

[53] Acharjee S, Sarmah BK. Biotechnologically generating 'super chickpea' for food and nutritional security. Plant Science: An International Journal of Experimental Plant Biology. 2013;**207**:108-116. PubMed PMID: 23602105. Epub 2013/04/23. eng

[54] Nnamani CV, Ajayi SA, Oselebe HO, Atkinson CJ, Igboabuchi AN, Ezigbo EC. *Sphenostylis stenocarpa* (ex. A. Rich.) Harms., a fading genetic resource in a changing climate: Prerequisite for conservation and sustainability. Plants (Basel, Switzerland). 2017;**6**(3):1-16.

PubMed PMID: 28704944. PMCID: PMC5620586. Epub 2017/07/15. eng

[55] Ogunsola KE, Ojuederie OB, Emmanuel B. In vitro morphogenic responses of African yam bean (*Sphenostylis stenocarpa* (Hochst ex. A. Rich.) Harms) accessions to plant growth regulators. *Plant Cell, Tissue and Organ Culture (PCTOC)*. 2016;**127**(3):613-622

[56] Adewale B, Vroh-Bi I, Dumet D, Nnadi S, Kehinde O, Ojo D, et al. Genetic diversity in African yam bean accessions based on AFLP markers: Towards a platform for germplasm improvement and utilization. *Plant Genetic Resources*. 2015;**13**(2):111-118

[57] Adewale DB, Adegbite AE. Investigation of the breeding mechanism of African yam bean [Fabaceae] (*Sphenostylis stenocarpa* Hochst. Ex. A. Rich) Harms. *Notulae Scientia Biologicae*. 2018;**10**(2):199-204

[58] Odongo FO, Oyoo ME, Wasike V, Owuoche JO, Karanja L, Korir P. Genetic diversity of Bambara groundnut (*Vigna subterranea* (L.) verdc.) landraces in Kenya using microsatellite markers. *The African Journal of Biotechnology*. 2015;**14**(4):283-291

[59] Molosiwa OO, Aliyu S, Stadler F, Mayes K, Massawe F, Kilian A, et al. SSR marker development, genetic diversity and population structure analysis of Bambara groundnut [*Vigna subterranea* (L.) Verdc.] landraces. *Genetic Resources and Crop Evolution*. 2015;**62**(8):1225-1243

[60] Bharatkumar C. Genetic Improvement of Bambara Groundnut (*Vigna subterranea* (L.) Verdc) Through Mutation Breeding. Bengaluru: University of Agricultural Sciences, GKVK; 2015

[61] Shashidhar H, Savithramma D. Genetic enhancement of protein

and methionine content in Bambara groundnut (*Vigna subterranea* (L.) Verdc.) through mutation breeding. *International Journal*. 2015;**8**

[62] Mubaiwa J, Fogliano V, Chidewe C, Linnemann AR. Bambara groundnut (*Vigna subterranea* (L.) Verdc.) flour: A functional ingredient to favour the use of an unexploited sustainable protein source. *PLoS One*. 2018;**13**(10):e0205776

[63] Bamba ASA. Beyond Landraces: Framework for the Genetic Improvement of Bambara Groundnut [*Vigna subterranea* (L.) Verdc.] for Global Food Security. United Kingdom: University of Nottingham; 2017

[64] Wong Q, Massawe F, Mayes K, Blythe M, Mayes S, editors. Molecular genetic tools to support genetic improvement of winged bean (*Psophocarpus tetragonolobus*) for food and nutrition security. In: XXIX International Horticultural Congress on Horticulture: Sustaining Lives, Livelihoods and Landscapes (IHC2014); 2014;**1110**:2016

[65] Wong Q, Massawe F, Mayes S, editors. Improving winged bean (*Psophocarpus tetragonolobus*) productivity: An analysis of the determinants of productivity. In: XXIX International Horticultural Congress on Horticulture: Sustaining Lives, Livelihoods and Landscapes (IHC2014); 2014;**1102**

[66] Wong QN, Tanzi AS, Ho WK, Malla S, Blythe M, Karunaratne A, et al. Development of gene-based SSR markers in winged bean (*Psophocarpus tetragonolobus* (L.) DC.) for diversity assessment. *Genes*. 2017;**8**(3):100

[67] Li F, Cao D, Liu Y, Yang T, Wang G. Transcriptome sequencing of lima bean (*Phaseolus lunatus*) to identify putative positive selection in *Phaseolus* and legumes. *International Journal of Molecular Sciences*. 2015;**16**(7):15172-15187

- [68] Laxmi K. SSR Marker Assay-based Polymorphism among the Dolichos Bean (*Lablab purpureus* L.) Germplasm Accessions Differing in Photoperiod-induced Sensitivity to Flowering Time. Bengaluru: University of Agricultural Sciences, GKVK; 2015
- [69] Zhang G, Xu S, Mao W, Gong Y, Hu Q. Development of EST-SSR markers to study genetic diversity in hyacinth bean (*Lablab purpureus* L.). Plant Omics. 2013;6(4):295
- [70] Kumar H, Gowda M, Ramesh S. Identification of cross legume species/genera SSR markers polymorphic to parents of recombinant inbred lines derived from two bi-parental crosses in dolichos bean (*Lablab purpureus* L. sweet). Mysore Journal of Agricultural Sciences. 2016;50(2):372-375
- [71] Rai KK, Rai N, Rai SP. Recent advancement in modern genomic tools for adaptation of *Lablab purpureus* L to biotic and abiotic stresses: Present mechanisms and future adaptations. Acta Physiologiae Plantarum. 2018;40(9):164
- [72] Yao LM, Wang B, Cheng LJ, Wu TL. Identification of key drought stress-related genes in the hyacinth bean. PLoS One. 2013;8(3):e58108
- [73] Oboh HA, Muzquiz M, Burbano C, Cuadrado C, Pedrosa MM, Ayet G, et al. Effect of soaking, cooking and germination on the oligosaccharide content of selected Nigerian legume seeds. Plant Foods for Human Nutrition (Dordrecht, Netherlands). 2000;55(2):97-110. PubMed PMID: 10898479. Epub 2000/07/18. eng
- [74] Viera Diaz J. Genetic improvement of legumes. Archivos Latinoamericanos de Nutrición. 1996;44(4 Suppl 1):41s-43s. PubMed PMID: 9221716. Epub 1996/12/01. Mejoramiento genetico de leguminosas. spa
- [75] Bohra A, Jha R, Pandey G, Patil PG, Saxena RK, Singh IP, et al. New hypervariable SSR markers for diversity analysis, hybrid purity testing and trait mapping in Pigeonpea [*Cajanus cajan* (L.) Millspaugh]. Frontiers in Plant Science. 2017;8:377. PubMed PMID: 28408910. PMCID: PMC5374739. Epub 2017/04/15. eng
- [76] Priyanka B, Sekhar K, Sunita T, Reddy VD, Rao KV. Characterization of expressed sequence tags (ESTs) of pigeonpea (*Cajanus cajan* L.) and functional validation of selected genes for abiotic stress tolerance in *Arabidopsis thaliana*. Molecular Genetics and Genomics : MGG. 2010;283(3):273-287. PubMed PMID: 20131066. Epub 2010/02/05. eng
- [77] Varshney RK, Chen W, Li Y, Bharti AK, Saxena RK, Schlueter JA, et al. Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers. Nature Biotechnology. 2012;30(1):83
- [78] Pontes Junior V, Melo P, Pereira H, Melo L. Genetic potential of common bean progenies obtained by different breeding methods evaluated in various environments. Embrapa Arroz e Feijão-Artigo em periódico indexado (ALICE). 2016;15(3):gmr15038622
- [79] Rodríguez De Luque JJ, Creamer B. Principal constraints and trends for common bean production and commercialization; establishing priorities for future research. Agronomía Colombiana. 2014;32(3):423-431
- [80] Blair M, Galeano C, Tovar E, Torres M, Velasco A, Beebe SE, et al. Development of a Mesoamerican intragenepool genetic map for QTL detection in a drought tolerant x susceptible common bean (*Phaseolus vulgaris* L.) cross. 2012;29:71-88
- [81] Baldermann S, Blagojević L, Frede K, Klopsch R, Neugart S, Neumann A,

- et al. Are neglected plants the food for the future? *Critical Reviews in Plant Sciences*. 2016;**35**(2):106-119
- [82] Dansi A, Vodouhè R, Azokpota P, Yedomonhan H, Assogba P, Adjatin A, et al. Diversity of the neglected and underutilized crop species of importance in Benin. *The Scientific World Journal*. 2012;**2012**:1-19
- [83] Padulosi S, Amaya K, Jäger M, Gotor E, Rojas W, Valdivia R. A holistic approach to enhance the use of neglected and underutilized species: The case of Andean grains in Bolivia and Peru. *Sustainability*. 2014;**6**(3):1283-1312
- [84] Fatokun C, Girma G, Abberton M, Gedil M, Unachukwu N, Oyatomi O, et al. Genetic diversity and population structure of a mini-core subset from the world cowpea (*Vigna unguiculata* (L.) Walp.) germplasm collection. *Scientific Reports*. 2018;**8**(1):16035
- [85] Boukar O, Fatokun CA, Huynh BL, Roberts PA, Close TJ. Genomic tools in cowpea breeding programs: Status and perspectives. *Frontiers in Plant Science*. 2016;**7**:757. PubMed PMID: 27375632. PMCID: PMC4891349. Epub 2016/07/05. eng
- [86] Saka J, Ajibade S, Adeniyani O, Olowoyo R, Ogunbodede B. Survey of underutilized grain legume production systems in the Southwest agricultural zone of Nigeria. *Journal of Agricultural and Food Information*. 2004;**6**(2-3):93-108
- [87] Chapman MA. Transcriptome sequencing and marker development for four underutilized legumes. *Applications in Plant Sciences*. 2015;**3**(2):1-5. PubMed PMID: 25699221. PMCID: PMC4332146. Epub 2015/02/24. eng
- [88] Cooper JW, Wilson MH, Derks MFL, Smit S, Kunert KJ, Cullis C, et al. Enhancing faba bean (*Vicia faba* L.) genome resources. *Journal of Experimental Botany*. 2017;**68**(8):1941-1953. PubMed PMID: 28419381. PMCID: PMC5429004. Epub 2017/04/19. eng
- [89] Obala J, Saxena RK, Singh VK, Kumar CVS, Saxena KB, Tongoona P, et al. Development of sequence-based markers for seed protein content in pigeonpea. *Molecular Genetics and Genomics: MGG*. 2019;**294**(1):57-68. PubMed PMID: 30173295. Epub 2018/09/03. eng
- [90] Kumawat G, Raje RS, Bhutani S, Pal JK, Mithra AS, Gaikwad K, et al. Molecular mapping of QTLs for plant type and earliness traits in pigeonpea (*Cajanus cajan* L. Millsp.). *BMC Genetics*. 2012;**13**:84. PubMed PMID: 23043321. PMCID: PMC3504571. Epub 2012/10/10. eng
- [91] Wu GA, Prochnik S, Jenkins J, Salse J, Hellsten U, Murat F, et al. Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. *Nature Biotechnology*. 2014;**32**(7):656-662. PubMed PMID: 24908277. PMCID: PMC4113729. Epub 2014/06/09. eng
- [92] Borlaug NE. Contributions of conventional plant breeding to food production. *Science (New York, N.Y.)*. 1983;**219**(4585):689-693. PubMed PMID: 17814030. Epub 1983/02/11. eng
- [93] Zargar SM, Mahajan R, Nazir M, Nagar P, Kim ST, Rai V, et al. Common bean proteomics: Present status and future strategies. *Journal of Proteomics*. 2017;**169**:239-248. PubMed PMID: 28347863. Epub 2017/03/30. eng
- [94] Jarquin D, Kocak K, Posadas L, Hyma K, Jedlicka J, Graef G, et al. Genotyping by sequencing for genomic prediction in a soybean breeding population. *BMC Genomics*. 2014;**15**:740.

PubMed PMID: 25174348. PMCID:
PMC4176594. Epub 2014/09/02. eng

[95] Takahashi Y, Somta P, Muto C, Iseki K, Naito K, Pandiyan M, et al. Novel genetic resources in the genus *Vigna* unveiled from gene bank accessions. *PLoS One*. 2016;**11**(1):e0147568

[96] Wojciechowski MF, Lavin M, Sanderson MJ. A phylogeny of legumes (Leguminosae) based on analysis of the plastid *matK* gene resolves many well-supported subclades within the family. *American Journal of Botany*. 2004;**91**(11):1846-1862

[97] Popoola J, Adebayo B, Adegbite A, Omonhinmin CA, Adewale B. Fruit morphometric and RAPD evaluation of intraspecific variability in some accessions of African yam bean (*Sphenostylis stenocarpa* Hochst. Ex. A. Rich. Harms). *Annual Research and Review in Biology*. 2017;**14**(4):1-10

[98] Morgante M, Olivieri A. PCR-amplified microsatellites as markers in plant genetics. *The Plant Journal*. 1993;**3**(1):175-182

[99] Saxena RK, von Wettberg E, Upadhyaya HD, Sanchez V, Songok S, Saxena K, et al. Genetic diversity and demographic history of *Cajanus* spp. illustrated from genome-wide SNPs. *PLoS One*. 2014;**9**(2):e88568. PubMed PMID: 24533111. PMCID: PMC3922937. Epub 2014/02/18. eng

[100] Mohanty CS, Verma S, Singh V, Khan S, Gaur P, Gupta P, et al. Characterization of winged bean (*Psophocarpus tetragonolobus* (L.) DC.) based on molecular, chemical and physiological parameters. *American Journal of Molecular Biology*. 2013;**3**(04):187

[101] Jackson SA, Iwata A, Lee SH, Schmutz J, Shoemaker R. Sequencing crop genomes: Approaches and

applications. *The New Phytologist*. 2011;**191**(4):915-925

[102] Parisod C, Alix K, Just J, Petit M, Sarilar V, Mhiri C, et al. Impact of transposable elements on the organization and function of allopolyploid genomes. *The New Phytologist*. 2010;**186**(1):37-45

[103] Meyers BC, Tingey SV, Morgante M. Abundance, distribution, and transcriptional activity of repetitive elements in the maize genome. *Genome Research*. 2001;**11**(10):1660-1676

[104] Jiang N, Bao Z, Zhang X, Eddy SR, Wessler SR. Pack-MULE transposable elements mediate gene evolution in plants. *Nature*. 2004;**431**(7008):569

[105] Bennetzen JL. Transposable elements, gene creation and genome rearrangement in flowering plants. *Current Opinion in Genetics and Development*. 2005;**15**(6):621-627

[106] Du J, Grant D, Tian Z, Nelson RT, Zhu L, Shoemaker RC, et al. SoyTEdb: A comprehensive database of transposable elements in the soybean genome. *BMC Genomics*. 2010;**11**:113. PubMed PMID: 20163715. PMCID: PMC2830986. Epub 2010/02/19. eng

[107] Singh A, Sharma AK, Singh NK, Sharma TR. PpTFDB: A pigeonpea transcription factor database for exploring functional genomics in legumes. *PLoS One*. 2017;**12**(6):e0179736. PubMed PMID: 28651001. PMCID: PMC5484553. Epub 2017/06/27. eng

[108] Abdelrahman M, Jogaiah S, Burritt DJ, Tran LSP. Legume genetic resources and transcriptome dynamics under abiotic stress conditions. *Plant, Cell and Environment*. Sep 2018;**41**(9):1972-1983

[109] Bonthala VS, Mayes K, Moreton J, Blythe M, Wright V, May ST,

et al. Identification of gene modules associated with low temperatures response in Bambara groundnut by network-based analysis. PLoS One. 2016;**11**(2):e0148771. PubMed PMID: 26859686. PMCID: PMC4747569. Epub 2016/02/10. eng

[110] Ribaut J, De Vicente M, Delannay X. Molecular breeding in developing countries: Challenges and perspectives. Current Opinion in Plant Biology. 2010;**13**(2):213-218

[111] Varshney RK, Glaszmann JC, Leung H, Ribaut JM. More genomic resources for less-studied crops. Trends in Biotechnology. 2010;**28**(9):452-460

[112] Tan H, Huang H, Tie M, Tang Y, Lai Y, Li H. Transcriptome profiling of two Asparagus bean (*Vigna unguiculata* subsp. *sesquipedalis*) cultivars differing in chilling tolerance under cold stress. PLoS One. 2016;**11**(3):e0151105. PubMed PMID: 26954786. PMCID: PMC4783050. Epub 2016/03/10. eng

[113] Ahmad NS, Redjeki ES, Ho WK, Aliyu S, Mayes K, Massawe F, et al. Construction of a genetic linkage map and QTL analysis in Bambara groundnut. Genome. 2016;**59**(7):459-472. PubMed PMID: 27253730. Epub 2016/06/03. eng

[114] Janila P, Nigam SN, Pandey MK, Nagesh P, Varshney RK. Groundnut improvement: Use of genetic and genomic tools. Frontiers in Plant Science. 2013;**4**:23. PubMed PMID: 23443056. PMCID: PMC3580887. Epub 2013/02/28. eng

[115] Saxena RK, Rathore A, Bohra A, Yadav P, Das RR, Khan AW, et al. Development and application of high-density Axiom Cajanus SNP array with 56K SNPs to understand the genome architecture of released cultivars and founder genotypes. The Plant Genome. 2018;**11**(3):1-10. PubMed PMID: 30512043. Epub 2018/12/05. eng